Appendix 1: Analysis Pipeline

This zip file contains two folders, this first 'Appendix_1_data_extraction_proccessing', contains code that:

1. Takes data from the COMPADRE Plant Matrix Database (R object downloaded on the 24th of October 2014 included in file) and filters out the populations that do not meet our selection criteria.

2. Calculates the four demographic metrics we focus on, Population growth rate (λ), temporal variation of λ (CV(λ)), damping ratio (ρ) and a composite variable for elasticities of λ (SPG).

3. Extract data from BioClim (http://worldclim.org/current) and Aridity Index (CGIAR-CSI GeoPortal; http://www.csi.cgiar.org) raster layers and perform PCA analysis on the relevant variables

4. Combine all the filtered data from COMPADRE with the demographic metrics and environmental variables and saves the resulting data frame as 'combined_bc_ai_all_responses.Rdata'

The second folder 'Appendix_1_model_code_and_plotting' contains code that takes the data frame in 'combined_bc_ai_all_responses.Rdata' and fits statistical models using JAGS 3.4.0-1. The statistical models used in the analysis are defined in the file 'non_elast_predict _models.R'. These models are called using the 'r2jags' interface in the file 'pop_metric _prediction.R'. the resulting model objects are saved and called by 'plotting_functions.R' to produce diagnostic and trace plots for the models, along with the results plots for the paper and Appendices.

WARNING: Several steps (in particular the BioClim data extraction and the MCMC sampling) take hours, days, or weeks to run. If one were to try and run this code as is, it will take a long time. Secondly this analysis pipeline has multiple steps, each of which requires several libraries and dependencies to work. It would be surprising if anybody could get it to work on the first attempt.